

#17



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,980B

DATE: 05/19/2003

TIME: 15:05:18

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\05192003\J019980B.raw

3 <110> APPLICANT: Berthelsen, Jens
 4 Toma, Salvatore
 5 Isacchi, Antonella
 W--> 6 <120> TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, And Methods
 Related To
 W--> 7 The Same
 W--> 8 <130> FILE REFERENCE: PHRM0373
 W--> 9 <140> CURRENT APPLICATION NUMBER: 10/019,980B
 C--> 10 <141> CURRENT FILING DATE: 2003-01-06
 11 <150> PRIOR APPLICATION NUMBER: 09/350,982
 12 <151> PRIOR FILING DATE: 1999-07-09
 13 <150> PRIOR APPLICATION NUMBER: PCT/EP00/06609
 14 <151> PRIOR FILING DATE: 2000-07-03
 W--> 15 <160> NUMBER OF SEQ ID: 10
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 18 <211> LENGTH: 20
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 20 <213> ORGANISM: Artificial Sequence
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 24 <400> SEQUENCE: 1
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 42 <213> ORGANISM: Homo sapiens
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 44 <221> NAME/KEY: misc_feature
 45 <222> LOCATION: (1124)..(1124)
 46 <223> OTHER INFORMATION: N is any nucleic acid
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 51 <223> OTHER INFORMATION: N is any nucleic acid
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 58 caacggggac gtggaacgag tcaagaggct ggtgacgcct gagaagggtga acagccgcga 180
 60 cacggcgggc aggaaatcca ccccgctgca cctcgccga ggttttgggc ggaaagacgt 240
 62 agttgaatat ttgcttcaga atgggtgcaa tgtccaagca cgtgatgatg ggggccttat 300
 64 tcctcttcat aatgcatgct cttttggtca tgcgaagta gtcaatctcc ttttgcgaca 360
 66 tgggtgcagac cccaatgctc gagataattg gaattatact cctctccatg aagctgcaat 420
 68 taaaggaaag attgatgttt gcattgtgct gttacagcat ggagctgagc caaccatccg 480
 70 aaatacacat ggaaggacag cattggattt agcagatcca tctgccaaag cagtgcctac 540
 72 tgggtgaatat aagaagatg aactcttaga aagtgccagg agtggcaatg aagaaaaaat 600
 74 gatggctcta ctcacaccat taaatgtcaa ctgccacgca agtgaatgga gaaagtcaac 660
 76 tccattacat ttggcagcag gatataacag agtaaaagatt gtacagctgt tactgcaaca 720
 78 tggagctgat gtccatgcta aagataaaag tgatctggta ccattacaca atgcctgttc 780
 80 ttatggctcat tatgaagtaa ctgaactttt ggtcaagcat ggtgcctgtg taaatgcaat 840
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 88 ctggttgctg caagctgcac gagaagctga tgttactcga atcaaaaaac atctctctct 1080
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 116 gcatggtgca gaccctacaa aaaaaaacag gtagggaaat actcctttgg atcttggtta 1920
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154 tattctcaag attcagaagg tttgtaacaa gaaactatgg gaaagataca ctcaccggag 3060
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158 tcctttttgtg aatgcaatta tccacaaagg cttttagtaa aggcattgctg acataggtgg 3180
160 tatgttttggg gctggcattt attttgcctg aaactcttcc aaaagcaatc aatatgtata 3240
162 tgggaattgga ggaggtactg ggtgtccagt tcacaaagac agatcttggt acatttgcca 3300
164 caggcagctg ctcttttgcc gggtaacctt gggaaagtct ttcctgcagt tcagtgcatt 3360
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172 ctaattccac tgaacctaaa atcatcaaag cagcagtggc ctctacgttt tactcctttg 3600
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184 aatacaattt catttgtaaa actgtaaata agagcttttg tactagccca gtatttattt 3960
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238	cgc aac ggg gac gtg gaa cga gtc aag agg ctg gtg acg cct gag aag	144
239	Arg Asn Gly Asp Val Glu Arg Val Lys Arg Leu Val Thr Pro Glu Lys	
240	35 40 45	
242	gtg aac agc cgc gac acg gcg ggc agg aaa tcc acc ccg ctg cac ctc	192
243	Val Asn Ser Arg Asp Thr Ala Gly Arg Lys Ser Thr Pro Leu His Leu	
244	50 55 60	
246	gcc gca ggt ttt ggg cgg aaa gac gta gtt gaa tat ttg ctt cag aat	240
247	Ala Ala Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn	
248	65 70 75 80	
250	ggt gca aat gtc caa gca cgt gat gat ggg ggc ctt att cct ctt cat	288
251	Gly Ala Asn Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His	
252	85 90 95	
254	aat gca tgc tct ttt ggt cat gct gaa gta gtc aat ctc ctt ttg cga	336
255	Asn Ala Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg	
256	100 105 110	
258	cat ggt gca gac ccc aat gct cga gat aat tgg aat tat act cct ctc	384
259	His Gly Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu	
260	115 120 125	
262	cat gaa gct gca att aaa gga aag att gat gtt tgc att gtg ctg tta	432
263	His Glu Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu	
264	130 135 140	
266	cag cat gga gct gag cca acc atc cga aat aca gat gga agg aca gca	480
267	Gln His Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala	
268	145 150 155 160	
270	ttg gat tta gca gat cca tct gcc aaa gca gtg ctt act ggt gaa tat	528
271	Leu Asp Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr	
272	165 170 175	
274	aag aaa gat gaa ctc tta gaa agt gcc agg agt ggc aat gaa gaa aaa	576
275	Lys Lys Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys	
276	180 185 190	
278	atg atg gct cta ctc aca cca tta aat gtc aac tgc cac gca agt gat	624
279	Met Met Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp	
280	195 200 205	
282	ggc aga aag tca act cca tta cat ttg gca gca gga tat aac aga gta	672
283	Gly Arg Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val	
284	210 215 220	
286	aag att gta cag ctg tta ctg caa cat gga gct gat gtc cat gct aaa	720
287	Lys Ile Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys	
288	225 230 235 240	
290	gat aaa ggt gat ctg gta cca tta cac aat gcc tgt tct tat ggt cat	768
291	Asp Lys Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His	
292	245 250 255	
294	tat gaa gta act gaa ctt ttg gtc aag cat ggt gcc tgt gta aat gca	816
295	Tyr Glu Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala	
296	260 265 270	
298	atg gac ttg tgg caa ttc act cct ctt cat gag gca gct tct aag aac	864

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 302 agg gtt gaa gta tgt tct ctt ctc tta agt tat ggt gca gac cca aca 912
 303 Arg Val Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr
 304 290 295 300
 306 ctg ctc aat tgt cac aat aaa agt gct ata gac ttg gct ccc aca cca 960
 307 Leu Leu Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro
 308 305 310 315 320
 310 cag tta aaa gaa aga tta gca tat gaa ttt aaa ggc cac tcg ttg ctg 1008
 311 Gln Leu Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu
 312 325 330 335
 314 caa gct gca cga gaa gct gat gtt act cga atc aaa aaa cat ctc tct 1056
 315 Gln Ala Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser
 316 340 345 350
 W--> 318 ctg gaa atg gtg aat ttc aag cat cct caa aca cat gaa aca gca ntg 1104
 319 Leu Glu Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Xaa
 320 355 360 365
 322 cat tgt gct gct gca tct cca tat ccc aaa aga aag caa ata tgt gaa 1152
 323 His Cys Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu
 324 370 375 380
 326 ctg ttg cta aga aaa gga gca amc atc aat gaa aag act aaa gaa ttc 1200
 327 Leu Leu Leu Arg Lys Gly Ala Xaa Ile Asn Glu Lys Thr Lys Glu Phe
 328 385 390 395 400
 330 ttg act cct ctg cac gtg gca tct gag aaa gct cat aat gat rtt gtt 1248
 331 Leu Thr Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Xaa Val
 332 405 410 415
 334 gaa gta gtg gtg aaa cat gaa gca aag gtt aat gct ctg gat aat ctt 1296
 335 Glu Val Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu
 336 420 425 430
 338 ggt cag act tct cta cac aga gct gca tat tgt ggt cat cta caa acc 1344
 339 Gly Gln Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr
 340 435 440 445
 342 tgc cgc cta ctc ctg agc tat ggg tgt gat cct aac att ata tcc ctt 1392
 343 Cys Arg Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu
 344 450 455 460
 346 cag ggc ttt act gct tta cag atg gga aat gaa aat gta cag caa ctc 1440
 347 Gln Gly Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu
 348 465 470 475 480
 350 ctc caa gag ggt atc tca tta ggt aat tca gag gca gac aga caa ttg 1488
 351 Leu Gln Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu
 352 485 490 495
 354 ctg gaa gct gca aag gct gga gat gtc gaa act gta aaa aaa ctg tgt 1536
 355 Leu Glu Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys
 356 500 505 510
 358 act gtt cag agt gtc aac tgc aga gac att gaa ggg cgt cag tct aca 1584
 359 Thr Val Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr
 360 515 520 525
 362 cca ctt cat ttt gca gct ggg tat aac aga gtg tcc gtg gtg gaa tat 1632
 363 Pro Leu His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1124,2672

Seq#:4; N Pos. 1102,2650

Seq#:4; Xaa Pos. 368,392,415,558,559,764,884

Seq#:5; Xaa Pos. 368,392,415,558,559,764,884

VERIFICATION SUMMARY

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Input Set : A:\PTO.VSK.txt

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L:6 M:283 W: Missing Blank Line separator, <120> field identifier
L:8 M:283 W: Missing Blank Line separator, <130> field identifier
L:9 M:283 W: Missing Blank Line separator, <140> field identifier
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:283 W: Missing Blank Line separator, <160> field identifier
L:17 M:283 W: Missing Blank Line separator, <210> field identifier
L:21 M:283 W: Missing Blank Line separator, <220> field identifier
L:32 M:283 W: Missing Blank Line separator, <220> field identifier
L:43 M:283 W: Missing Blank Line separator, <220> field identifier
L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1080
M:341 Repeated in SeqNo=3
L:211 M:283 W: Missing Blank Line separator, <220> field identifier
L:224 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:217
L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1056
M:341 Repeated in SeqNo=4
L:531 M:283 W: Missing Blank Line separator, <220> field identifier
L:669 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:352
M:341 Repeated in SeqNo=5
L:881 M:283 W: Missing Blank Line separator, <220> field identifier
L:892 M:283 W: Missing Blank Line separator, <220> field identifier
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L:914 M:283 W: Missing Blank Line separator, <220> field identifier
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